AMENDMENTS TO THE SPECIFICATION

Please amend page 3, line 25 through page 4, line 14, as follows:

Figure 2 depicts a partial labeling of adenosine in a DNA subsample in accordance with one embodiment of the disclosed methods and devices and an exemplary method for constructing a nucleotide time map **310, 320, 330, 340** (as shown in Figure 3) for one type of labeled nucleotide **220**, based on measured times between labeled nucleotides **220** in a number of complementary nucleic acid strands **230, 240, 250**. The times between labeled nucleotides **220** may be compiled into a time map **310, 320, 330, 340** (as shown in Figure 3) for each type of nucleotides labeled as described herein. Distances between the labelled nucleotides 220 may then be calculated from these time maps **310, 320, 330, 340** (as shown in Figure 3). The sequence **210** of the complementary strand **230, 240, 250** is shown, along with exemplary locations for labeled nucleotides **220**. As indicated **260**, where identical nucleotides are located adjacent to each other, this will be detected as an increased frequency of labeling at that location;

Figure 3 depicts how a complementary DNA sequence **210** may be assembled by aligning the four nucleotide time separation maps **310, 320, 330, 340** according to the non-overlapping rules. The template nucleic acid 200 will be an exact complement of the determined sequence **210**. Computerized and statistical tools can assist in this process.

Figure 4 depicts an exemplary method for constructing **450** time maps **310, 320, 330, 340** (as shown in Figure 3) for labeled nucleotides **220**.

Figure 5 illustrates an exemplary method for aligning **520** time maps **310, 320, 330, 340** (as shown in Figure 3) to obtain a nucleic acid sequence **200** of the complementary strand **210**.